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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/727,084DATE: 04/11/97
TIME: 14:08:13

INPUT SET: S16960.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Pulst, Stefan M.

(ii) TITLE OF INVENTION: NUCLEIC ACID ENCODING SPINOCEREBELLAR
ATAXIA-2 AND PRODUCTS RELATED THERETO

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Pretty, Schroeder & Poplawski

(B) STREET: 444 South Flower Street, Suite 2000

(C) CITY: Los Angeles

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 90071

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" diskette

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/727,084

(B) FILING DATE: October 8, 1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Viviana Amzel, Ph. D.

(B) REGISTRATION NUMBER: 30930

(C) REFERENCE/DOCKET NUMBER: P07 37217

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 213-622-7700

(B) TELEFAX: 213-489-4210

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: both

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/727,084DATE: 04/11/97
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47 (D) TOPOLOGY: both

48

49 (ii) MOLECULE TYPE: DNA (genomic)

50

51

52

53 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

54

55 TTGGTAGCAA CGGAAACGGC GGCGGCGCGT TTCGGCCCCG CTCCCGGCGG CTCCTTGGTC 60

56

57 TCGGCGGGCC TCCCCGCCCC TTCGTGCTCG TCCTTCTCCC CCTCGCCAGC CCGGGCGCCC 120

58

59 CTCCGGCCGC GCCAACCCGC GCCTCCCCGC TCGGCGCCCC TGCCTCCCCG CCGCGTTCCG 180

60

61 GCGTCTCCTT GGCGCGCCCC GCTCCCGGCT GTCCCCGCCC GGCGTGCGAG CCGGTGTATG 240

62

63 GGCCCTCAC CATGTCGCTG AAGCCCCAGC AGCAGCAGCA GCAGCAGCAG CAACAGCAGC 300

64

65 AGCAGCAACA GCAGCAGCAG CAGCAGCAGC AGCCGCCGCC CGCGGCTGCC AATGTCCGCA 360

66

67 AGCCCGGCGG CAGCGGCCTT CTAGCGTCGC CCGCCGCCGC GCCTTCGCCG TCCTCGTCCT 420

68

69 CCGTCTCCTC GTCCTCGGCC ACGGCTCCCT CCTCGGTGGT CGCGGCGACC TCCGGCGGCG 480

70

71 GGAGGCCCCG CCTGGGCAGG TGGGTGTCGG CACCCC 516

72

73 (2) INFORMATION FOR SEQ ID NO:2:

74

75 (i) SEQUENCE CHARACTERISTICS:

76

77 (A) LENGTH: 4481 base pairs

78

79 (B) TYPE: nucleic acid

80

81 (C) STRANDEDNESS: both

82

83 (D) TOPOLOGY: both

84

85 (ii) MOLECULE TYPE: cDNA

86

87

88

89 (ix) FEATURE:

90

91 (A) NAME/KEY: CDS

92

93 (B) LOCATION: 163..4101

94

95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

96

97 ACCCCCGAGA AAGCAACCCA GCGCGCCGCC CGCTCCTCAC GTGTCCCTCC CGGCCCCGGG 60

98

99 GCCACCTCAC GTTCTGCTTC CGTCTGACCC CTCCGACTTC CGGTAAAGAG TCCCTATCCG 120

100

101 CACCTCCGCT CCCACCCGGC GCCTCGGCGC GCCCGCCCTC CG ATG CGC TCA GCG 174

102

103 Met Arg Ser Ala

104

105 GCC GCA GCT CCT CGG AGT CCC GCG GTG GCC ACC GAG TCT CGC CGC TTC 222

106

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100	Ala	Ala	Ala	Pro	Arg	Ser	Pro	Ala	Val	Ala	Thr	Glu	Ser	Arg	Arg	Phe	
101	5					10					15					20	
102																	
103	GCC	GCA	GCC	AGG	TGG	CCC	GGG	TGG	CGC	TCG	CTC	CAG	CGG	CCG	GCG	CGG	270
104	Ala	Ala	Ala	Arg	Trp	Pro	Gly	Trp	Arg	Ser	Leu	Gln	Arg	Pro	Ala	Arg	
105				25						30					35		
106																	
107	CGG	AGC	GGG	CGG	GGC	GGC	GGT	GGC	GCG	GCC	CCG	GGA	CCG	TAT	CCC	TCC	318
108	Arg	Ser	Gly	Arg	Gly	Gly	Gly	Gly	Ala	Ala	Pro	Gly	Pro	Tyr	Pro	Ser	
109				40					45					50			
110																	
111	GCC	GCC	CCT	CCC	CCG	CCC	GGC	CCC	GGC	CCC	CCT	CCC	TCC	CGG	CAG	AGC	366
112	Ala	Ala	Pro	Pro	Pro	Pro	Gly	Pro	Gly	Pro	Pro	Pro	Ser	Arg	Gln	Ser	
113			55					60					65				
114																	
115	TCG	CCT	CCC	TCC	GCC	TCA	GAC	TGT	TTT	GGT	AGC	AAC	GGC	AAC	GGC	GGC	414
116	Ser	Pro	Pro	Ser	Ala	Ser	Asp	Cys	Phe	Gly	Ser	Asn	Gly	Asn	Gly	Gly	
117		70					75					80					
118																	
119	GGC	GCG	TTT	CGG	CCC	GGC	TCC	CGG	CGG	CTC	CTT	GGT	CTC	GGC	GGG	CCT	462
120	Gly	Ala	Phe	Arg	Pro	Gly	Ser	Arg	Arg	Leu	Leu	Gly	Leu	Gly	Gly	Pro	
121	85					90				95						100	
122																	
123	CCC	CGC	CCC	TTC	GTC	GTC	GTC	CTT	CTC	CCC	CTC	GCC	AGC	CCG	GGC	GCC	510
124	Pro	Arg	Pro	Phe	Val	Val	Val	Leu	Leu	Pro	Leu	Ala	Ser	Pro	Gly	Ala	
125				105						110					115		
126																	
127	CCT	CCG	GCC	GCG	CCA	ACC	CGC	GCC	TCC	CCG	CTC	GGC	GCC	CGT	GCG	TCC	558
128	Pro	Pro	Ala	Ala	Pro	Thr	Arg	Ala	Ser	Pro	Leu	Gly	Ala	Arg	Ala	Ser	
129			120					125					130				
130																	
131	CCG	CCG	CGT	TCC	GGC	GTC	TCC	TTG	GCG	CGC	CCG	GCT	CCC	GGC	TGT	CCC	606
132	Pro	Pro	Arg	Ser	Gly	Val	Ser	Leu	Ala	Arg	Pro	Ala	Pro	Gly	Cys	Pro	
133			135					140					145				
134																	
135	CGC	CCG	GCG	TGC	GAG	CCG	GTG	TAT	GGG	CCC	CTC	ACC	ATG	TCG	CTG	AAG	654
136	Arg	Pro	Ala	Cys	Glu	Pro	Val	Tyr	Gly	Pro	Leu	Thr	Met	Ser	Leu	Lys	
137		150					155					160					
138																	
139	CCC	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CAA	CAG	CAG	CAG	CAG	CAA	CAG		702
140	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	
141	165					170				175						180	
142																	
143	CAG	CAG	CAG	CAG	CAG	CAG	CAG	CCG	CCG	CCC	GCG	GCT	GCC	AAT	GTC	CGC	750
144	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala	Ala	Ala	Asn	Val	Arg	
145				185						190					195		
146																	
147	AAG	CCC	GGC	GGC	AGC	GGC	CTT	CTA	GCG	TCG	CCC	GCC	GCC	GCG	CCT	TCG	798
148	Lys	Pro	Gly	Gly	Ser	Gly	Leu	Leu	Ala	Ser	Pro	Ala	Ala	Ala	Pro	Ser	
149			200						205					210			
150																	
151	CCG	TCC	TCG	TCC	TCG	GTC	TCC	TCG	TCC	TCG	GCC	ACG	GCT	CCC	TCC	TCG	846
152	Pro	Ser	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ser	Ala	Thr	Ala	Pro	Ser	Ser	

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153	215	220	225	
154				
155	GTG GTC GCG GCG ACC TCC GGC GGC GGG AGG CCC GGC CTG GGC AGA GGT			894
156	Val Val Ala Ala Thr Ser Gly Gly Gly Arg Pro Gly Leu Gly Arg Gly			
157	230	235	240	
158				
159	CGA AAC AGT AAC AAA GGA CTG CCT CAG TCT ACG ATT TCT TTT GAT GGA			942
160	Arg Asn Ser Asn Lys Gly Leu Pro Gln Ser Thr Ile Ser Phe Asp Gly			
161	245	250	255	260
162				
163	ATC TAT GCA AAT ATG AGG ATG GTT CAT ATA CTT ACA TCA GTT GTT GGC			990
164	Ile Tyr Ala Asn Met Arg Met Val His Ile Leu Thr Ser Val Val Gly			
165	265	270	275	
166				
167	TCC AAA TGT GAA GTA CAA GTG AAA AAT GGA GGT ATA TAT GAA GGA GTT			1038
168	Ser Lys Cys Glu Val Gln Val Lys Asn Gly Gly Ile Tyr Glu Gly Val			
169	280	285	290	
170				
171	TTT AAA ACT TAC AGT CCG AAG TGT GAT TTG GTA CTT GAT GCC GCA CAT			1086
172	Phe Lys Thr Tyr Ser Pro Lys Cys Asp Leu Val Leu Asp Ala Ala His			
173	295	300	305	
174				
175	GAG AAA AGT ACA GAA TCC AGT TCG GGG CCG AAA CGT GAA GAA ATA ATG			1134
176	Glu Lys Ser Thr Glu Ser Ser Gly Pro Lys Arg Glu Glu Ile Met			
177	310	315	320	
178				
179	GAG AGT ATT TTG TTC AAA TGT TCA GAC TTT GTT GTG GTA CAG TTT AAA			1182
180	Glu Ser Ile Leu Phe Lys Cys Ser Asp Phe Val Val Val Gln Phe Lys			
181	325	330	335	340
182				
183	GAT ATG GAC TCC AGT TAT GCA AAA AGA GAT GCT TTT ACT GAC TCT GCT			1230
184	Asp Met Asp Ser Ser Tyr Ala Lys Arg Asp Ala Phe Thr Asp Ser Ala			
185	345	350	355	
186				
187	ATC AGT GCT AAA GTG AAT GGC GAA CAC AAA GAG AAG GAC CTG GAG CCC			1278
188	Ile Ser Ala Lys Val Asn Gly Glu His Lys Glu Lys Asp Leu Glu Pro			
189	360	365	370	
190				
191	TGG GAT GCA GGT GAA CTC ACA GCC AAT GAG GAA CTT GAG GCT TTG GAA			1326
192	Trp Asp Ala Gly Glu Leu Thr Ala Asn Glu Glu Leu Glu Ala Leu Glu			
193	375	380	385	
194				
195	AAT GAC GTA TCT AAT GGA TGG GAT CCC AAT GAT ATG TTT CGA TAT AAT			1374
196	Asn Asp Val Ser Asn Gly Trp Asp Pro Asn Asp Met Phe Arg Tyr Asn			
197	390	395	400	
198				
199	GAA GAA AAT TAT GGT GTA GTG TCT ACG TAT GAT AGC AGT TTA TCT TCG			1422
200	Glu Glu Asn Tyr Gly Val Val Ser Thr Tyr Asp Ser Ser Leu Ser Ser			
201	405	410	415	420
202				
203	TAT ACA GTG CCC TTA GAA AGA GAT AAC TCA GAA GAA TTT TTA AAA CGG			1470
204	Tyr Thr Val Pro Leu Glu Arg Asp Asn Ser Glu Glu Phe Leu Lys Arg			
205	425	430	435	

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SEQUENCE VERIFICATION REPORT
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Original Text